



# Local initiation conditions for water autoionization

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The pH of liquid water is determined by the infrequent process in which water molecules split into short-lived hydroxide and hydronium ions. This reaction is difficult to probe experimentally and challenging to simulate. One of the open questions is whether the local water structure around a slightly stretched OH bond is actually initiating the eventual breakage of this bond or whether this event is driven by a global ordering that involves many water molecules far away from the reaction center. Here, we investigated the self-ionization of water at room temperature by rare-event ab initio molecular dynamics and obtained autoionization rates and activation energies in good agreement with experiments. Based on the analysis of thousands of molecular trajectories, we identified a couple of local order parameters and show that if a bond stretch occurs when all these parameters are around their ideal range, the chance for the first dissociation step (double-proton jump) increases from  $10^{-7}$  to 0.4. Understanding these initiation triggers might ultimately allow the steering of chemical reactions.

autoionization | water | path sampling | machine learning |  
ab initio molecular dynamics

**A**mong all possible chemical reactions that occur in water, the most fundamental is the water dissociation reaction (1), which is of major importance in many areas of chemistry and biology (2). Water plays an important role as a universal solvent for a wide variety of chemical processes and can act both as an acid and as a base. In aqueous solution, water will self-ionize and form hydroxide ( $\text{OH}^-$ ) and hydronium ( $\text{H}_3\text{O}^+$ ) ions which take on Eigen- or Zundel-like structures (2–6). Experiments show that the mean lifetime for an individual molecule before undergoing autoionization is about 11 h (7, 8).

The autoionization event has not been directly probed by experiments and the dissociation rate is obtained using the water dissociation equilibrium constant and the rate for the much faster recombination reaction (7, 8). The experimental challenges make the autoionization event a pertinent target for computer simulations for which previous constrained ab initio simulations have given important information about the mechanism (9–11). However, the use of constraints leads to a loss of the spontaneous dynamics of the system and the selection of a reaction coordinate that accurately measures the progress of the reaction is challenging. These limitations can be avoided by path-sampling methods such as transition path sampling (TPS) (12) or replica exchange transition interface sampling (RETIS) (13, 14) which are specifically designed for sampling rare events without altering the dynamics while less influenced by the choice of the order parameter (15). Geissler et al. (16) applied TPS with ab initio molecular dynamics (MD) to simulate just 10 uncorrelated autoionization events and demonstrated that the mechanism involves transfer of protons along a hydrogen bond wire with concomitant breaking of the wire. In their work, local solvent properties (e.g., ion coordination numbers and the presence of specific hydrogen bonds) were used to interpret the destabilization that leads to ionization. The absence of clear visually observable correlations led to the conclusion that the destabilization is caused by rare electric-field fluctuations which arise primarily from long-range electrostatic interactions and thus that

local order parameters are not suitable to describe the event. Hassanali et al. (17) studied the reverse recombination reaction (i.e., neutralization of ionized water molecules) with standard ab initio MD and reported that this event takes place by a collective compression of the water wire bridging the ions, followed by a triple concerted proton jump. The  $\text{OH}^-$  ion which is neutralized remains in a hypercoordinated state and Hassanali et al. (17) hypothesized that it could serve, together with the compression of the wire, as a nucleation site for autoionization. This view opposes the statement of Geissler et al. (16) that the dissociation event is primarily triggered by nonlocal structural fluctuations. We note that concerted proton transfers and collective compression of water wires have also been observed for the recombination of a weak base in water (18).

Both of these studies give important information about the autoionization mechanism, although they do not unambiguously reveal the conditions that need to accompany a bond stretch fluctuation to initiate the reaction. In this work, we aim to tackle this ambiguity and quantitatively identify initiation conditions for water autoionization. Simulating the dissociation events may not be sufficient as the apparent initiation conditions observed in trajectories that lead to dissociation may also be present in trajectories with an initial bond stretch but still fail to dissociate. Also nonreactive or “almost reactive” trajectories contain important information as these allow for identification of effective initiation conditions that really matter: those that discriminate

## Significance

The dissociation of water is arguably the most fundamental chemical reaction occurring in the aqueous phase. Despite that the splitting of a water molecule very seldom occurs, the reaction is of major importance in many areas of chemistry and biology. Direct experimental probing of the event is still impossible and also simulating the event via accurate computer simulations is challenging. Here, we achieved the latter via specialized rare-event algorithms estimating rates of dissociation in agreement with indirect experimental measurements. Even more interestingly, by a rigorous analysis of our results we identified anomalies in the water structure that act as initiators of the reaction, a finding that suggests paradigms for steering and catalyzing chemical reactions.

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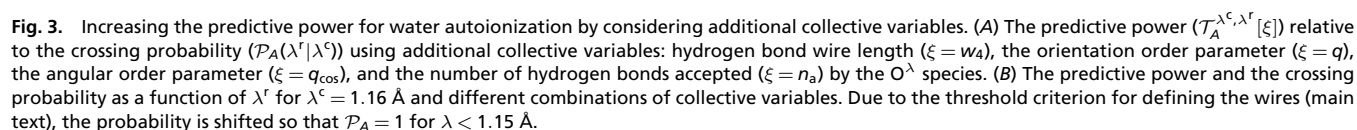
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## Conclusions

We investigated the autoionization of water at room temperature, using an unconstrained *ab initio* rare-event simulation method. Our simulations sample reactive events that happen on the timescale of minutes and we demonstrated that autoionization can be initiated by the hypercoordination of a stretched OH bond and the compression of a hydrogen bond wire as suggested by Hassalani et al. (17). However, these are not sufficient conditions. Only when the wire is strongly condensed ( $<7.3$  Å) and the stretched OH bond accepts four hydrogen bonds, does the reaction probability become significant (0.15), but only 0.6% of the reactive trajectories start off with such extreme conditions. The vast majority of reactive paths start with milder initial values for these two parameters. In this region of parameter space the reaction probability is largely enhanced compared with an arbitrary case, but still extremely small. Hence, the reaction takes place when additional structural parameters have values inside the right range. We identified additional structural parameters which correspond to the alignment of the hydrogen bond wire and the distortion from a tetrahedral arrangement. Hence, we showed that the local order parameters can be used to predict the self-ionization event, although it requires a combination of several conditions.

Due to the multiple correlated factors that influence the water autoionization, we combined our analysis method with ML techniques which identified additional parameters not considered before, in particular the O–H stretch of the oxygen closest to  $O^\lambda$ . Even though the ML result did not outperform the level of predictiveness by the human effort based on intuition, visual inspection of many molecular movies, and intensive trial-and-error approaches, the ML approach found all previously identified parameters very efficiently and, in addition, revealed some equally important parameters that were overlooked. We therefore believe that ML applied to path sampling has a great potential especially since data limitations will become less of an issue in the future due to the further expected increase of high-performance computing, a better parallelization scheme of sampling unequal trajectory-length path ensembles, and the use of more efficient Monte Carlo (MC) path-generating moves (37). It would therefore be promising to apply the same method to other aqueous-phase chemistry studies which so far have mainly been based on biased dynamics (31, 38).

The fundamental understanding of reaction triggers that can be gathered by this approach could open up avenues of practical applications. For instance, even if not all identified parameters correlating with reactivity will necessarily imply causal correlation, it is plausible that an intelligent manipulation of their equilibrium distribution via external electric fields (39) or inclusion of additives might lead to catalytic ways to steer reactions and in particular water dissociation.

## Materials and Methods

**Simulation Methods.** The MD simulations required by the RETIS algorithm (14) were performed with the Born–Oppenheimer MD capabilities of the CP2K program package (40). We used the Becke–Lee–Yang–Parr (BLYP) functional with a DZVP-MOLOPT (41) basis set and a plane-wave cutoff of 280 Ry. The BLYP functional gives a reasonable description of the structure and dynamics of liquid water (42, 43) and the absence of dispersion corrections (44) is likely of minor importance for ion–water interactions where the dominant interactions are mainly electrostatic. However, we note that the BLYP functional is known to give an overstructured description of liquid water with a low diffusion coefficient (45). Previous studies on the recombination mechanism for water (17, 46) and for weak bases in water (18) have, however, found that the collective compression of the hydrogen bond wire and the motion of the protons are reproduced with different choices of the functional and basis set.

The initial system consisted of 32 water molecules placed in a cubic simulation box of  $9.85 \times 9.85 \times 9.85$  Å<sup>3</sup>. All MD simulations were carried out

under constant energy (microcanonical) dynamics, with a time step of 0.5 fs and periodic boundaries.

The transition region was divided into 20 path ensembles by positioning RETIS interfaces at  $\lambda = \{1.07, 1.10, 1.13, 1.16, 1.19, 1.22, 1.25, 1.28, 1.31, 1.34, 1.39, 1.43, 1.48, 1.52, 1.56, 1.60, 2.00, 2.50, 2.90, 3.29\}$  Å. In addition, a final interface was placed at  $\lambda = \infty$  such that all trajectories were propagated until they reached the pure water state again. After generating an initial path for each path ensemble (this was done by repeatedly modifying the momenta of the particles and evolving the system forward in time until valid paths were obtained) the RETIS algorithm attempts to either swap paths between different path ensembles or generate new trajectories by the so-called shooting or the time-reversal move. In our simulations the probability of performing a swapping move was set to 50% while the probabilities of the two other moves were both set to 25%. New velocities for the shooting move were drawn from a Maxwell–Boltzmann distribution corresponding to an average temperature of 300 K.

We performed 24,000 MC moves for each path ensemble, using the RETIS algorithm. This generated between 8,000 and 18,000 distinct trajectories in each path ensemble. The length of the trajectories ranged from 13.5 fs to 1,365 fs and we disregarded the first 400 trajectories in our analysis.

**Analysis of Trajectories.** Crossing probabilities along the reaction coordinate  $\lambda$  were computed by matching the results of the different path ensembles. Projection of the crossing probability along  $\lambda'$  was obtained using the reweighting scheme of Rogal et al. (21) for the path ensembles in the transition interface sampling framework.

For trajectories harvested with the RETIS algorithm we calculated additional collective variables: the hydrogen bond wire length ( $w_i$ ), the number of hydrogen bond donors ( $n_d$ ) and acceptors ( $n_a$ ), the orientation order parameter ( $q$ ), and the angle formed by  $O^\lambda$  and its closest oxygen neighbors ( $q_{\cos}$ ). Using the first configuration in each trajectory, hydrogen atoms were assigned to the closest oxygen atom and this defined the initial H<sub>2</sub>O molecules. Then, the hydrogen bond network was obtained for each configuration in the trajectory. Hydrogen bonds were identified using the criteria of Luzar and Chandler (47) and all (shortest) hydrogen bond connections between all pairs of water molecules were determined using the Floyd–Warshall algorithm (48). This allowed us to represent the hydrogen bond structure as a graph. Next, the oxygen atom ( $O^\lambda$ ) used in the definition of the order parameter was identified. With no OH<sup>−</sup> present, this is the oxygen atom for which the covalent O–H distance is largest and when we have OH<sup>−</sup> present in the system, this is the OH<sup>−</sup> oxygen atom. After identifying  $O^\lambda$ , we obtained the number of hydrogen bonds accepted ( $n_a$ ) and donated ( $n_d$ ) by the water species containing it. The relevant hydrogen bond wire was obtained using the following criteria: (i) The wire should contain the oxygen atom used for the order parameter (identified as explained above) when the order parameter first crossed 1.15 Å, (ii) the wire should contain  $i$  water species, and (iii) the wire should be the shortest of the wires where two criteria  $i$  and  $ii$  are met. The length of the wire was defined as the sum of the O–O distances of consecutive molecules in the wire.

The orientation order parameter measures the distortion from a tetrahedral orientation of four water molecules around a central molecule and is defined by (27, 28)

$$q = 1 - \frac{3}{8} \sum_{j=1}^3 \sum_{k=j+1}^4 \left( \cos \psi_{jk} + \frac{1}{3} \right)^2 \quad [3]$$

Here,  $\psi_{jk}$  is the angle formed by the central oxygen and its four nearest oxygen neighbors. The central oxygen is always  $O^\lambda$  or the oxygen with the largest OH bond for pure water or the OH<sup>−</sup> oxygen if it is present. For a perfect tetrahedral orientation  $q = 1$  and it is  $q \neq 1$  otherwise. The angle order parameter,  $q_{\cos}$ , was obtained directly as  $q_{\cos} = \min(\cos \alpha, \cos \beta)$ , where  $\alpha$  and  $\beta$  are the two internal angles in the wire.

After calculating these additional collective variables, we analyzed the trajectories using the methodology of van Erp et al. (19). For the analysis we used 100 subinterfaces for both  $\lambda^r$  and  $\lambda^c$  for the range  $0 < \lambda/\text{Å} < 6.4$ . The histograms in the collective variable space were constructed using 20 bins for  $4.0 \leq w_3/\text{Å} \leq 7.0$ ,  $7.0 \leq w_4/\text{Å} \leq 9.6$ ,  $9.0 \leq w_5/\text{Å} \leq 12$ ; 20 bins for  $0 \leq q \leq 1$ ; and 25 bins for  $-1 \leq q_{\cos} \leq 1$ , while the bins (midpoints) were placed at  $-0.5, 0.5, 1.5, \dots, 6.5$  for both  $n_d$  and  $n_a$ .

The classification models were constructed using CARTs (20) available within the R (49) software package. The mean of sensitivity and specificity was used as the classifier performance measure (50).

For the CART models we considered several sets of collective variables and we obtained these variables at the frame in the trajectories where the order parameter first crossed 1.15 Å. The trajectories were classified as reactive if they reached a  $\lambda \geq 2$  and as nonreactive otherwise. The first set of collective variables consisted of all 4,560 atom–atom separations in the system, which gave a model in which the oxygen–oxygen distances were most important. This model did not lend itself to an easy interpretation and we next considered several models with a reduced number of collective variables.

In the best-performing model (performance measure for training 0.89 and for testing 0.88) we considered 138 collective variables: all oxygen–hydrogen distances for initially bound water molecules, all oxygen–oxygen distances involving  $O^{\lambda}$ , the averaged distances between  $O^{\lambda}$  and its  $i = \{2, 3, \dots, 31\}$  oxygen neighbors, the cosine of all angles formed by  $O^{\lambda}$

and its 4 closest oxygen neighbors, all of the collective variables considered in the predictive power analysis, and the Steinhardt order parameters of order 3, 4, and 6 (32). When performing the predictive power analysis for the collective variables used by the CART analysis, we used 20 bins in the range [0.7, 2.0] for oxygen–hydrogen distances and 20 bins in the range [1.0, 4.2] for oxygen–oxygen distances, and for angles and the Steinhardt order parameters we used similar bins to those for  $q_{\cos}$  and  $q$  given above.

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